

Table S6: QTL of CIM analysis across TEs. Chromosome (Chr.), position (Pos.), support interval (SI), p-value, proportion of phenotypic variance explained (R^2), and additive effects (Eff) of the founders Event (A), BAYP4535 (B), Ambition (C), Firl3565 (D), Format (E), Potenzial (F) and Bussard (G) relative to Julius are given for the traits powdery mildew (PM), septoria tritici blotch (STB), tan spot (TS), plant height (PH), ear emergence time (EET) and leaf angle distribution (LAD). The detection of a QTL within a TE is specified (TE), additionally.

Trait	Chr.	Pos. (cM)	SI (cM)	P-value	R^2 *	Eff(A)	Eff(B)	Eff(C)	Eff(D)	Eff(E)	Eff(F)	Eff(G)	TE
PM [1-9]					36.0								
	1A	3	3-3	6.4E-15	9.4	-2.2	-3.5	-1.1	NA	-2.0	-2.5	-2.7	17FS1
	1A	63	62-63	1.4E-05	3.2	1.8	2.4	2.1	1.6	2.4	2.8	3.5	17FS1
	5A	281	280-282	1.1E-04	3.8	-0.9	-0.7	-1.3	-1.0	-0.8	-1.5	-0.6	17FS1
	6B	217	217-217	2.0E-08	6.2	-1.7	-0.5	-0.8	0.2	0.2	-1.7	-1.1	16RG, 17FS1
	7A	382	381-382	2.9E-10	12.8	-2.3	-0.8	-2.5	-1.1	-0.8	-0.8	-1.4	16RG, 17FS1
STB [%]					23.5								
	1B	356	346-356	3.9E-04	5.4	7.2	1.9	3.7	-3.5	-0.3	-16.6	-12.5	17FS1
	2B	71	71-81	4.8E-04	4.0	-1.8	6.9	-8.5	21.8	11.2	1.4	-7.7	17FS1
	2B	243	234-252	4.1E-05	6.3	33.8	-3.7	-6.0	-19.0	11.8	7.7	8.3	16FS1, 17FS1
	2D	20	20-21	6.1E-09	8.5	-10.6	-9.7	0.7	-7.4	11.7	-12.0	3.5	16FS1, 17FS1
TS [%]					29.9								
	1A	23	23-23	4.1E-04	6.8	12.5	1.9	3.7	NA	2.2	5.2	14.0	
	2A	90	83-93	5.0E-05	6.6	7.0	1.0	2.4	5.8	4.1	0.1	-5.7	
	2B	222	217-232	3.0E-06	8.3	-10.6	-0.3	16.8	NA	4.1	9.7	4.8	16FS2, 17FS2
	3D	81	81-84	8.2E-04	6.8	-8.6	-10.8	-5.9	-2.6	3.0	-7.0	-2.9	
	7A	148	146-154	2.2E-06	10.6	0.9	-6.5	-3.5	5.3	1.9	-0.2	1.8	
PH [cm]					54.6								
	4B	68	68-69	0.0E+00	9.2	3.2	-8.4	NA	0.4	4.0	1.7	2.4	16FS2, 17FS2, 17SL
	4D	27	27-27	0.0E+00	33.6	-4.5	14.3	3.0	27.8	14.5	5.3	NA	16FS1, 16FS2, 17FS1, 17FS2, 17SL
	6A	159	155-160	5.3E-14	11.7	-1.1	-0.9	-10.5	-4.0	-3.4	-7.9	0.9	16FS1, 16FS2, 17FS1, 17FS2, 17SL
EET [DaM]					26.6								
	3A	105	95-115	3.3E-04	2.8	-0.9	-1.1	-0.9	-0.2	-0.9	-1.8	-1.1	
	3A	230	223-230	8.4E-06	8.8	-0.9	0.4	1.0	1.7	1.9	0.1	0.2	
	5A	182	180-184	5.3E-04	7.4	1.0	0.2	0.5	0.3	-0.2	1.3	1.0	17FS1, 17FS2
	5B	100	94-104	2.9E-06	6.5	0.9	2.1	0.3	-0.3	0.8	0.2	0.4	16FS2, 17SL
	7A	80	79-80	6.9E-05	3.4	-1.0	0.2	-1.6	-1.7	-1.6	-1.0	-1.5	16FS2

Table S6 (Continuation): QTL of CIM analysis across TEs. Chromosome (Chr.), position (Pos.), support interval (SI), p-value, proportion of phenotypic variance explained (R^2), and additive effects (Eff) of the founders Event (A), BAYP4535 (B), Ambition (C), Firl3565 (D), Format (E), Potenzial (F) and Bussard (G) relative to Julius are given for the traits powdery mildew (PM), septoria tritici blotch (STB), tan spot (TS), plant height (PH), ear emergence time (EET) and leaf angle distribution (LAD). The detection of a QTL within a TE is specified (TE), additionally.

Trait	Chr.	Pos. (cM)	SI (cM)	P-value	R^2 *	Eff(A)	Eff(B)	Eff(C)	Eff(D)	Eff(E)	Eff(F)	Eff(G)	TE
LAD [1-9]					24.8								
	2B	176	174-176	5.1E-13	14.3	-2.1	0.8	0.5	0.6	0.0	1.7	NA	16FS1
	2D	167	162-167	8.7E-05	5.6	-1.2	0.6	0.3	0.5	0.5	0.9	0.9	17FS1
	6A	40	36-46	2.9E-06	6.6	-0.2	0.5	-0.6	0.3	-0.9	0.3	-1.0	

* For each trait the explained phenotypic variance of the model fitting all detected QTL simultaneously is given in bold values above the individual R^2 values for each QTL.